RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/826,115 TIME: 15:06:08

Input Set : A:\Pto.amc
Output Set: N:\CRF3\04232001\I826115.raw

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     4 <110> APPLICANT: Chang, Gwong-Jen J
     6 <120> TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
     7       Flavivirus Infection
     9 <130> FILE REFERENCE: 14114.0332U3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/826,115
C--> 11 <141> CURRENT FILING DATE: 2001-04-04 .
    11 <150> PRIOR APPLICATION NUMBER: pct/us99/12298
    12 <151> PRIOR FILING DATE: 1999-06-03
    14 <150> PRIOR APPLICATION NUMBER: 09/701,536
    15 <151> PRIOR FILING DATE: 2000-11-29
    17 <150> PRIOR APPLICATION NUMBER: 60/087,908
    18 <151> PRIOR FILING DATE: 1998-06-04
    20 <160> NUMBER OF SEQ ID NOS: 31
    22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    24 <210> SEQ ID NO: 1 ·
    25 <211> LENGTH: 48
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Artificial Sequence
    29 <220> FEATURE:
    30 <223> OTHER INFORMATION: Description of artificial sequence; note =
    31       synthetic construct
    33 <221> NAME/KEY: CDS
    34 <222> LOCATION: (25)...(48)
    36 <221> NAME/KEY: misc_feature
    37 <222> LOCATION: 1-48
    38 <223> OTHER INFORMATION: Amplimer 14DV389
    40 <400> SEQUENCE: 1
    41 cttggtacct ctagagccgc cgcc atg ggc aga aag caa aac aaa aga          48
    42                          Met Gly Arg Lys Gln Asn Lys Arg
    43                           1               5
    46 <210> SEQ ID NO: 2
    47 <211> LENGTH: 8
    48 <212> TYPE: PRT
    49 <213> ORGANISM: Artificial Sequence
    51 <220> FEATURE:
    52 <223> OTHER INFORMATION: Description of artificial sequence; note =
    53       synthetic construct
    55 <400> SEQUENCE: 2
    56 Met Gly Arg Lys Gln Asn Lys Arg
    57  1               5
    59 <210> SEQ ID NO: 3
    60 <211> LENGTH: 50
    61 <212> TYPE: DNA
    62 <213> ORGANISM: Artificial Sequence
    64 <220> FEATURE:
    65 <223> OTHER INFORMATION: Description of artificial sequence; note =
    66       synthetic construct
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 68 <221> NAME/KEY: misc_feature
 69 <222> LOCATION: 1-50
 70 <223> OTHER INFORMATION: Amplimer c14DV2453
 72 <400> SEQUENCE: 3
 73 ttttcttttg cggccgctca aacttaagca tgcacattgg tcgctaagaa              50
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 48
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Artificial Sequence
 80 <220> FEATURE:
 81 <223> OTHER INFORMATION: Description of artificial sequence; note =
 82       synthetic construct
 84 <221> NAME/KEY: CDS
 85 <222> LOCATION: (25)...(48)
 87 <221> NAME/KEY: misc_feature
 88 <222> LOCATION: (1)...(48)
 89 <223> OTHER INFORMATION: Amplimer YFDV389
 91 <400> SEQUENCE: 4
 92 cttggtacct ctagagccgc cgcc atg cgt tcc cat gat gtt ctg act         48
 93                           Met Arg Ser His Asp Val Leu Thr
 94                           1               5
 97 <210> SEQ ID NO: 5
 98 <211> LENGTH: 8
 99 <212> TYPE: PRT
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Description of artificial sequence; note =
104       synthetic construct
106 <400> SEQUENCE: 5
107 Met Arg Ser His Asp Val Leu Thr
108 1               5
110 <210> SEQ ID NO: 6
111 <211> LENGTH: 41
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of artificial sequence; note =
117       synthetic construct
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: 1-41
121 <223> OTHER INFORMATION: Amplimer cYFDV2452
123 <400> SEQUENCE: 6
124 ttttcttttg cggccgctca cgccccaact cctagagaaa c                       41
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 51
128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of artificial sequence; note =
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133       synthetic construct
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (25)...(51)
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: 1-51
140 <223> OTHER INFORMATION: Amplimer SLEDV410
142 <400> SEQUENCE: 7
143 cttggtacct ctagagccgc cgcc atg tct aaa aaa aga gga ggg acc aga       51
144                            Met Ser Lys Lys Arg Gly Gly Thr Arg
145                             1                   5
148 <210> SEQ ID NO: 8
149 <211> LENGTH: 9
150 <212> TYPE: PRT
151 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Description of artificial sequence; note =
155       synthetic construct
157 <400> SEQUENCE: 8
158 Met Ser Lys Lys Arg Gly Gly Thr Arg
159  1               5
161 <210> SEQ ID NO: 9
162 <211> LENGTH: 38
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Description of artificial sequence; note =
168       synthetic construct
170 <221> NAME/KEY: misc_feature
171 <222> LOCATION: 1-38
172 <223> OTHER INFORMATION: Amplimer cSLEDV2449
174 <400> SEQUENCE: 9
175 ttttcttttg cggccgctta ggcttgcacg ctggttgc                           38
177 <210> SEQ ID NO: 10
178 <211> LENGTH: 7500
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of artificial sequence; note =
184       synthetic construct
186 <221> NAME/KEY: CDS
187 <222> LOCATION: (916)...(3009)
189 <221> NAME/KEY: misc_feature
190 <222> LOCATION: 1-7500
191 <223> OTHER INFORMATION: pCDJE 2-7
193 <400> SEQUENCE: 10
194 gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg    60
195 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg   120
196 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc   180
197 ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt   240
```

```
198 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata    300
199 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc    360
200 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc    420
201 attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt    480
202 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt    540
203 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca    600
204 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg    660
205 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc    720
206 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg    780
207 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca    840
208 ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc    900
209 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa    951
210              Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
211               1               5                    10
213 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg    999
214 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
215         15                  20                  25
217 gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc   1047
218 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
219      30                  35                  40
221 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga   1095
222 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
223  45                  50                  55                  60
225 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag   1143
226 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
227              65                  70                  75
229 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca   1191
230 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
231          80                  85                  90
233 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat   1239
234 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
235          95                  100                 105
237 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg   1287
238 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
239      110                 115                 120
241 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct   1335
242 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
243 125                 130                 135                 140
245 tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac   1383
246 Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn
247              145                 150                 155
249 tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc   1431
250 Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly
251              160                 165                 170
253 tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc   1479
254 Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu
255          175                 180                 185
257 ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc   1527
258 Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly
```

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259     190                  195                    200
261 aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg    1575
262 Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu
263 205                  210                    215                 220
265 gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca    1623
266 Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro
267               225                    230                    235
269 aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag    1671
270 Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu
271               240                    245                    250
273 gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg    1719
274 Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val
275         255                    260                    265
277 gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat    1767
278 Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp
279         270                    275                    280
281 agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac    1815
282 Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn
283 285                  290                    295                 300
285 gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc    1863
286 Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe
287               305                    310                    315
289 tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc    1911
290 Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile
291               320                    325                    330
293 aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac    1959
294 Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn
295         335                    340                    345
297 cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt    2007
298 His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe
299         350                    355                    360
301 aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac    2055
302 Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr
303 365                  370                    375                 380
305 gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa    2103
306 Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu
307               385                    390                    395
309 gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg    2151
310 Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg
311               400                    405                    410
313 gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca    2199
314 Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr
315         415                    420                    425
317 gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc    2247
318 Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala
319         430                    435                    440
321 aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat    2295
322 Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His
323 445                  450                    455                 460
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VERIFICATION SUMMARY ·   DATE: 04/23/2001
PATENT APPLICATION: US/09/826,115   TIME: 15:06:09

Input Set : **A:\Pto.amc**
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date